

# スズキ目ノトセニア亜目魚類における細胞呼吸関連遺伝子の特異的な分子進化

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## Unique molecular evolution of genes involved in the cellular respiration system in notothenioid fishes

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It has been shown that the evolutionary rates are faster in notothenioid fishes for some mitochondrial genes involved in oxidative phosphorylation of cellular respiration (Papetti et al. 2007). To further understand this unique feature of molecular evolution in cellular respiration system, we have investigated mitochondrial and nuclear genes of Antarctic and Patagonian toothfish from molecular evolutionary viewpoints.

So far we have determined the nucleotide sequence of entire mitochondrial genome of Antarctic toothfish (*Dissostichus mawsoni*) except control regions and of most mitochondrial genes of Patagonian toothfish (*D. eleginoides*). Nucleotide sequences of 24 nuclear genes involved in oxidative phosphorylation of cellular respiration were also determined through the analyses of Antarctic toothfish spleen RNA by next generation sequencer, with supplementing publically available EST data of Antarctic toothfish. Conducting molecular evolutionary analyses of notothenioid mitochondrial genes together with those of Perciformes, it was shown that the evolutionary rates were faster for notothenioids in the genes coding the subunits of ATP synthase (Fig. 1-a) or NADH dehydrogenase (Fig. 1-b), confirming previous report by Papetti et al. Moreover essentially similar results were obtained for the nuclear genes coding some subunits of ATP synthase in the analyses using a limited number of Actinopterygii genes (Fig. 2). Overall, these analyses show that the increase of evolutionary rates was not limited to some mitochondrial genes but also observed among the nuclear genes coding subunits of ATP synthase. Furthermore, when the numbers of nonsynonymous nucleotide substitutions per nonsynonymous sites ( $dn$ ) were compared with the numbers of synonymous nucleotide substitutions per synonymous sites ( $ds$ ), it was shown that the ratios of  $dn/ds$  tended to be larger in notothenioids (data not shown), even though the ratios were less than one. These results raise a possibility that relaxation of functional constraint in ATP synthase have caused the faster evolutionary rate of notothenioid genes.

### Reference

C. Papetti, P. Liò, L. Rüber, T. Patarnello and R. Zardoya, Antarctic Fish Mitochondrial Genomes Lack *ND6* Gene, *J Mol Evol*, 65, 519-528, 2008.

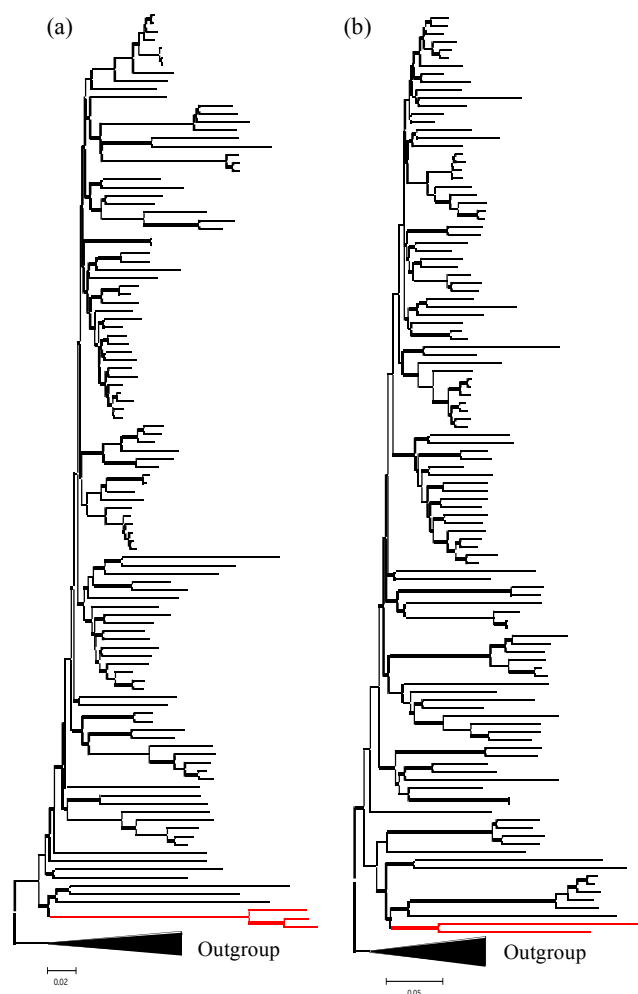


Figure 1. Phylogenetic trees of (a) ATP8/6 and (b) ND6 genes of Perciformes inferred by NJ method using p-distance. Those indicated in red are the lineage leading to notothenioids. Outgroup sequences used were of Osteoglossiformes.

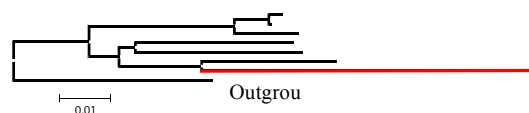


Figure 2. Phylogenetic trees of ATP  $\delta$  inferred by NJ method using p-distance. Outgroup sequence used was of *Danio rerio*.